



74 4

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

Applicant : Rachel Meyers
Serial No. : 09/801,267
Filed : Herewith 3/6/01
Title : 26583, A NOVEL SERINE/THREONINE PHOSPHATASE AND USES THEREFOR

Art Unit : Unknown
Examiner : Unknown

Box Patent Application

Commissioner for Patents
Washington, D.C. 20231

STATEMENT UNDER 37 CFR §1.821(f)

I hereby state, as required by 37 C.F.R. §1.821(f), that the content of the paper and computer-readable copy of the Sequence Listing, submitted in accordance with 37 C.F.R. §§1.821(c) and (e), respectively, are the same.

Respectfully submitted,

Date: July 5, 2001

Diana M. Collazo
Diana M. Collazo
Reg. No. 46,635

Fish & Richardson P.C.
225 Franklin Street
Boston, MA 02110-2804
Telephone: (617) 542-5070
Facsimile: (617) 542-8906

20181994.doc

CERTIFICATE OF MAILING BY FIRST CLASS MAIL

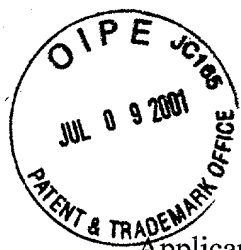
I hereby certify under 37 CFR §1.8(a) that this correspondence is being deposited with the United States Postal Service as first class mail with sufficient postage on the date indicated below and is addressed to the Commissioner for Patents, Washington, D.C. 20231.

July 6, 2001
Date of Deposit

Maria Reen
Signature

Maria Reen
Typed or Printed Name of Person Signing Certificate

09801267.070901



IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

Applicant : Rachel Meyers
Serial No. : 09/801,267
Filed : March 6, 2001
Title : 26583, A NOVEL SERINE/THREONINE PHOSPHATASE AND USES THEREFOR

Art Unit : 1645
Examiner : Unknown

Box Missing Parts

Commissioner for Patents
Washington, D.C. 20231

VERIFIED STATEMENT UNDER 37 CFR §1.821(f)

I, Jennifer H. Payne, declare that I personally prepared the paper and the computer-readable copy of the Sequence Listing filed herewith for the above-identified application and that the content of both is the same.

I further declare that all statements made herein of my own knowledge are true and that all statements made on information and belief are believed to be true; and false statements and the like so made are punishable by fine or imprisonment, or both, under Section 1001 of Title 18 of The United States Code, and that such willful false statements may jeopardize the validity of the application or any patent issued thereon.

Date:

July 5, 2001

Jennifer H. Payne

Fish & Richardson P.C.
225 Franklin Street
Boston, MA 02110-2804
Telephone: (617) 542-5070
Facsimile: (617) 542-8906
20174889.doc

CERTIFICATE OF MAILING BY FIRST CLASS MAIL

I hereby certify under 37 CFR §1.8(a) that this correspondence is being deposited with the United States Postal Service as first class mail with sufficient postage on the date indicated below and is addressed to the Commissioner for Patents, Washington, D.C. 20231.

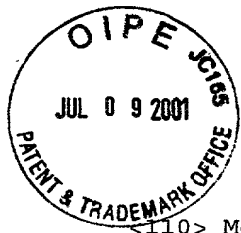
Date of Deposit

July 6, 2001

Signature

Maria Keen
Maria Keen

Typed or Printed Name of Person Signing Certificate



SEQUENCE LISTING

<110> Meyers, Rachel A.

<120> 26583, A NOVEL SERINE/THREONINE
PHOSPHATASE AND USES THEREFOR

<130> 10448-025001

<150> US 60/187,454

<151> 2000-03-07

<160> 5

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 2838

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (462)...(2072)

<221> misc_feature

<222> (1)...(2838)

<223> n = A,T,C or G

<400> 1

ggttttccac	gttttgontg	accctgtttg	ctcaactrwc	ktytktktyk	ykttytstkt	60
trygcssykw	yamrakmymm	rmkttkaaaa	amcmrraaag	ttaaytggtg	agtttagtct	120
ttttgtcttt	tattttcaagg	ttccggatcc	gggtgggtgg	caaatacaaag	aactgctcct	180
cagtggatgt	tgcctttact	tctaggcctg	tacggaagtg	ttacttctgc	tctaaaagct	240
gcggaattct	aatacgactc	actataggga	gtcgacccac	gcgtccgggtg	ggcaggccgg	300
gggtgagggc	tgcgctccg	ggagctgcac	ggggctgcgt	ggaaagagcg	ccgagcgggtg	360
gcgtcgttgt	cgtccctcc	tcgtcgggaa	gaatcgtttg	gtctcctgcc	gtgcccggaa	420
ttccagtcag	aagttccagc	ctgccactgt	tctctgatgc	c atg cca gca cca act		476
				Met Pro Ala Pro Thr		
				1	5	

caa ctg ttt ttt cct ctc atc cgt aac tgt gaa ctg agc agg atc tat	524
Gln Leu Phe Phe Pro Leu Ile Arg Asn Cys Glu Leu Ser Arg Ile Tyr	
10 15 20	

ggc act gca tgt tac tgc cac cac aaa cat ctc tgt tgt tcc tca tcg	572
Gly Thr Ala Cys Tyr Cys His His Lys His Leu Cys Cys Ser Ser Ser	
25 30 35	

tac att cct cag agt cga ctg aga tac aca cct cat cca gca tat gct	620
Tyr Ile Pro Gln Ser Arg Leu Arg Tyr Thr Pro His Pro Ala Tyr Ala	
40 45 50	

acc ttt tgc agg cca aag gag aac tgg tgg cag tac acc caa gga agg	668
Thr Phe Cys Arg Pro Lys Glu Asn Trp Trp Gln Tyr Thr Gln Gly Arg	
55 60 65	

aga tat gct tcc aca cca cag aaa ttt tac ctc aca cct cca caa gtc	716
Arg Tyr Ala Ser Thr Pro Gln Lys Phe Tyr Leu Thr Pro Pro Gln Val	

0930469.03004

70	75	80	85	
aat agc atc ctt aaa gct aat gaa tac agt ttc aaa gtg cca gaa ttt				764
Asn Ser Ile Leu Lys Ala Asn Glu Tyr Ser Phe Lys Val Pro Glu Phe	90	95	100	
gac ggc aaa aat gtc agt tct atc ctt gga ttt gac agc aat cag ctg				812
Asp Gly Lys Asn Val Ser Ser Ile Leu Gly Phe Asp Ser Asn Gln Leu	105	110	115	
cct gca aat gca ccc att gag gac cgg aga agt gca gca acc tgc ttg				860
Pro Ala Asn Ala Pro Ile Glu Asp Arg Arg Ser Ala Ala Thr Cys Leu	120	125	130	
cag acc aga ggg atg ctt ttg ggg gtt ttt gat ggc cat gca ggt tgt				908
Gln Thr Arg Gly Met Leu Leu Gly Val Phe Asp Gly His Ala Gly Cys	135	140	145	
gct tgt tcc cag gca gtc agt gaa aga ctc ttt tat tat att gct gtc				956
Ala Cys Ser Gln Ala Val Ser Glu Arg Leu Phe Tyr Tyr Ile Ala Val	150	155	160	165
tct ttg tta ccc cat gag act ttg cta gag att gaa aat gca gtg gag				1004
Ser Leu Leu Pro His Glu Thr Leu Leu Glu Ile Glu Asn Ala Val Glu	170	175	180	
agc ggc cgg gca ctg cta ccc att ctc cag tgg cac aag cac ccc aat				1052
Ser Gly Arg Ala Leu Leu Pro Ile Leu Gln Trp His Lys His Pro Asn	185	190	195	
gat tac ttt agt aag gag gca tcc aaa ttg tac ttt aac agc ttg agg				1100
Asp Tyr Phe Ser Lys Glu Ala Ser Lys Leu Tyr Phe Asn Ser Leu Arg	200	205	210	
act tac tgg caa gag ctt ata gac ctc aac act ggt gag tcg act gat				1148
Thr Tyr Trp Gln Glu Leu Ile Asp Leu Asn Thr Gly Glu Ser Thr Asp	215	220	225	
att gat gtt aag gag gct cta att aat gcc ttc aag agg ctt gat aat				1196
Ile Asp Val Lys Glu Ala Leu Ile Asn Ala Phe Lys Arg Leu Asp Asn	230	235	240	245
gac atc tcc ttg gag gcg caa gtt ggt gat cct aat tct ttt ctc aac				1244
Asp Ile Ser Leu Glu Ala Gln Val Gly Asp Pro Asn Ser Phe Leu Asn	250	255	260	
tac ctg gtg ctt cga gtg gca ttt tct gga gcc act gct tgt gtg gcc				1292
Tyr Leu Val Leu Arg Val Ala Phe Ser Gly Ala Thr Ala Cys Val Ala	265	270	275	
cat gtg gat ggt gtt gac ctt cat gtg gcc aat act ggc gat agc aga				1340
His Val Asp Gly Val Asp Leu His Val Ala Asn Thr Gly Asp Ser Arg	280	285	290	
gcc atg ctg ggt gtg cag gaa gag gac ggc tca tgg tca gca gtc acg				1388
Ala Met Leu Gly Val Gln Glu Glu Asp Gly Ser Trp Ser Ala Val Thr	295	300	305	
ctg tct aat gac cac aat gct caa aat gaa aga gaa cta gaa cgg ctg				1436
Leu Ser Asn Asp His Asn Ala Gln Asn Glu Arg Glu Leu Glu Arg Leu	310	315	320	325

aaa ttg gaa cat cca aag agt gag gcc aag agt gtc gtg aaa cag gat	1484
Lys Leu Glu His Pro Lys Ser Glu Ala Lys Ser Val Val Lys Gln Asp	
330 335 340	
cgg ctg ctt ggc ttg ctg atg cca ttt agg gca ttt gga gat gta aag	1532
Arg Leu Leu Gly Leu Leu Met Pro Phe Arg Ala Phe Gly Asp Val Lys	
345 350 355	
ttc aaa tgg agc att gac ctt caa aag aga gtg ata gaa tct ggc cca	1580
Phe Lys Trp Ser Ile Asp Leu Gln Lys Arg Val Ile Glu Ser Gly Pro	
360 365 370	
gac cag ttg aat gac aat gaa tat acc aag ttt att cct cct aat tat	1628
Asp Gln Leu Asn Asp Asn Glu Tyr Thr Lys Phe Ile Pro Pro Asn Tyr	
375 380 385	
cac aca cct cct tat ctc act gct gag cca gag gta act tac cac cga	1676
His Thr Pro Pro Tyr Leu Thr Ala Glu Pro Glu Val Thr Tyr His Arg	
390 395 400 405	
tta agg cca cag gat aag ttt ctg gtg ttg gct act gat ggg ttg tgg	1724
Leu Arg Pro Gln Asp Lys Phe Leu Val Leu Ala Thr Asp Gly Leu Trp	
410 415 420	
gag act atg cat agg cag gat gtg gtt agg att gtg ggt gag tac cta	1772
Glu Thr Met His Arg Gln Asp Val Val Arg Ile Val Gly Glu Tyr Leu	
425 430 435	
act ggc atg cat cac caa cag cca ata gct gtt ggt ggc tac aag gtg	1820
Thr Gly Met His His Gln Gln Pro Ile Ala Val Gly Gly Tyr Lys Val	
440 445 450	
act ctg gga cag atg cat ggc ctt tta aca gaa agg aga acc aaa atg	1868
Thr Leu Gly Gln Met His Gly Leu Leu Thr Glu Arg Arg Thr Lys Met	
455 460 465	
tcc tcg gta ttt gag gat cag aac gca gca acc cat ctc att cgc cac	1916
Ser Ser Val Phe Glu Asp Gln Asn Ala Ala Thr His Leu Ile Arg His	
470 475 480 485	
gct gtg ggc aac aac gag ttt ggg act gtt gat cat gag cgc ctc tct	1964
Ala Val Gly Asn Asn Glu Phe Gly Thr Val Asp His Glu Arg Leu Ser	
490 495 500	
aaa atg ctt agt ctt cct gaa gag ctt gct cga atg tac aga gat gac	2012
Lys Met Leu Ser Leu Pro Glu Glu Leu Ala Arg Met Tyr Arg Asp Asp	
505 510 515	
att aca atc att gta gtt cag ttc aat tct cat gtt gta ggg gcg tat	2060
Ile Thr Ile Ile Val Val Gln Phe Asn Ser His Val Val Gly Ala Tyr	
520 525 530	
caa aac caa gaa tagtgagtgg ctctttcact ggcaattctc aaatgatata	2112
Gln Asn Gln Glu	
535	
catttaaagg gcagattttt taaaaagata ctactataat aaacattttcc agttgggtcat	2172
tctaagcatt tacccttttg atactctagc tagtcaggta ctccaaattg actttgcagc	2232
agggtggcag ggtcaggaga gtctggtcct gcctagctca gatttcatgg cacctgcact	2292
tgaagcaagt cacttcttta tcacaggtgt cttgaaacat tagcttcttt taccaacctg	2352

```

agaaaattag gatgacctgg caaataagat cttgaatagg ccaaaagcaa gtatcttgct 2412
gtgtgtagtc tcttggttaa agtgaagaaa cagtactgtt cacacctttc ttcactgaga 2472
ttccagtgtg catgagaaca tatattttatt ksmwkrwttt yywrrtacac agtctatgca 2532
ttwttcataw wmwtttttt twgcctaaat aargtkkttw wcamatcyag tthwtcmatc 2592
matraacras mamcaascaa tctrtatctr tttttkktkw trwttrwytg rmakgmwtsy 2652
twaktrrrak ramtawmcwc mstyatccay ccgmyykyt wmykwaaktr attgaaatat 2712
tttttwtttt gccccccct tggagtcagg aagggttttt agttttatct tctyttctat 2772
tgaagttaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 2832
ggcgaa 2838

```

```

<210> 2
<211> 537
<212> PRT
<213> Homo sapiens

```

```

<400> 2
Met Pro Ala Pro Thr Gln Leu Phe Phe Pro Leu Ile Arg Asn Cys Glu
 1          5          10          15
Leu Ser Arg Ile Tyr Gly Thr Ala Cys Tyr Cys His His Lys His Leu
          20          25          30
Cys Cys Ser Ser Ser Tyr Ile Pro Gln Ser Arg Leu Arg Tyr Thr Pro
          35          40          45
His Pro Ala Tyr Ala Thr Phe Cys Arg Pro Lys Glu Asn Trp Trp Gln
          50          55          60
Tyr Thr Gln Gly Arg Arg Tyr Ala Ser Thr Pro Gln Lys Phe Tyr Leu
          65          70          75          80
Thr Pro Pro Gln Val Asn Ser Ile Leu Lys Ala Asn Glu Tyr Ser Phe
          85          90          95
Lys Val Pro Glu Phe Asp Gly Lys Asn Val Ser Ser Ile Leu Gly Phe
          100          105          110
Asp Ser Asn Gln Leu Pro Ala Asn Ala Pro Ile Glu Asp Arg Arg Ser
          115          120          125
Ala Ala Thr Cys Leu Gln Thr Arg Gly Met Leu Leu Gly Val Phe Asp
          130          135          140
Gly His Ala Gly Cys Ala Cys Ser Gln Ala Val Ser Glu Arg Leu Phe
          145          150          155          160
Tyr Tyr Ile Ala Val Ser Leu Leu Pro His Glu Thr Leu Leu Glu Ile
          165          170          175
Glu Asn Ala Val Glu Ser Gly Arg Ala Leu Leu Pro Ile Leu Gln Trp
          180          185          190
His Lys His Pro Asn Asp Tyr Phe Ser Lys Glu Ala Ser Lys Leu Tyr
          195          200          205
Phe Asn Ser Leu Arg Thr Tyr Trp Gln Glu Leu Ile Asp Leu Asn Thr
          210          215          220
Gly Glu Ser Thr Asp Ile Asp Val Lys Glu Ala Leu Ile Asn Ala Phe
          225          230          235          240
Lys Arg Leu Asp Asn Asp Ile Ser Leu Glu Ala Gln Val Gly Asp Pro
          245          250          255
Asn Ser Phe Leu Asn Tyr Leu Val Leu Arg Val Ala Phe Ser Gly Ala
          260          265          270
Thr Ala Cys Val Ala His Val Asp Gly Val Asp Leu His Val Ala Asn
          275          280          285
Thr Gly Asp Ser Arg Ala Met Leu Gly Val Gln Glu Glu Asp Gly Ser
          290          295          300
Trp Ser Ala Val Thr Leu Ser Asn Asp His Asn Ala Gln Asn Glu Arg
          305          310          315          320
Glu Leu Glu Arg Leu Lys Leu Glu His Pro Lys Ser Glu Ala Lys Ser
          325          330          335
Val Val Lys Gln Asp Arg Leu Leu Gly Leu Leu Met Pro Phe Arg Ala
          340          345          350
Phe Gly Asp Val Lys Phe Lys Trp Ser Ile Asp Leu Gln Lys Arg Val

```

```

      355      360      365
Ile Glu Ser Gly Pro Asp Gln Leu Asn Asp Asn Glu Tyr Thr Lys Phe
      370      375      380
Ile Pro Pro Asn Tyr His Thr Pro Pro Tyr Leu Thr Ala Glu Pro Glu
385      390      395      400
Val Thr Tyr His Arg Leu Arg Pro Gln Asp Lys Phe Leu Val Leu Ala
      405      410      415
Thr Asp Gly Leu Trp Glu Thr Met His Arg Gln Asp Val Val Arg Ile
      420      425      430
Val Gly Glu Tyr Leu Thr Gly Met His His Gln Gln Pro Ile Ala Val
      435      440      445
Gly Gly Tyr Lys Val Thr Leu Gly Gln Met His Gly Leu Leu Thr Glu
450      455      460
Arg Arg Thr Lys Met Ser Ser Val Phe Glu Asp Gln Asn Ala Ala Thr
465      470      475      480
His Leu Ile Arg His Ala Val Gly Asn Asn Glu Phe Gly Thr Val Asp
      485      490      495
His Glu Arg Leu Ser Lys Met Leu Ser Leu Pro Glu Glu Leu Ala Arg
      500      505      510
Met Tyr Arg Asp Asp Ile Thr Ile Ile Val Val Gln Phe Asn Ser His
      515      520      525
Val Val Gly Ala Tyr Gln Asn Gln Glu
      530      535

```

```

<210> 3
<211> 1611
<212> DNA
<213> Homo sapiens

```

```

<400> 3
atgccagcac caactcaact gttttttcct ctcatccgta actgtgaact gagcaggatc      60
tatggcactg catgttactg ccaccacaaa catctctgtt gttcctcatc gtacattcct      120
cagagtcgac tgagatacac acctcatcca gcatatgcta ccttttgcag gccaaaggag      180
aactgggtggc agtacacca aggaaggaga tatgcttcca caccacagaa attttacctc      240
acacctccac aagtcaatag catccttaaa gctaataaat acagtttcaa agtgccagaa      300
tttgacggca aaaatgtcag ttctatcctt ggatttgaca gcaatcagct gcctgcaaatt      360
gcacccattg aggaccggag aagtgcagca acctgcttgc agaccagagg gatgcttttg      420
gggggtttttg atggccatgc aggttgtgct tgttcccagg cagtcagtga aagactcttt      480
tattatattg ctgtctcttt gttaccccat gagactttgc tagagattga aaatgcagtg      540
gagagcggcc gggcactgct acccattctc cagtggcaca agcaccocaa tgattacttt      600
agtaaggagg catccaaatt gtactttaac agcttgagga cttactggca agagcttata      660
gacctcaaca ctggtgagtc gactgatatt gatgttaagg aggtctaat taatgccttc      720
aagaggcttg ataatagcat ctccttggag gcgcaagttg gtgatcctaa ttcttttctc      780
aactacctgg tgccttcagat ggcattttct ggagccactg cttgtgtggc ccatgtggat      840
ggtgttgacc ttcatgtggc caatactggc gatagcagag ccatgctggg tgtgcaggaa      900
gaggacggct catggctcagc agtcacgctg tctaataacc acaatgctca aaatgaaaga      960
gaactagaac ggctgaaatt ggaacatcca aagagtgagg ccaagagtgt cgtgaaacag      1020
gatcggtgct ttggcttgcg gatgccattt agggcatttg gagatgtaaa gttcaaatgg      1080
agcattgacc ttcaaaaagag agtgatagaa tctggcccag accagttgaa tgacaatgaa      1140
tataccaagt ttattctctc taattatcac acacctcctt atctcactgc tgagccagag      1200
gtaactttacc accgattaag gccacaggat aagtttctgg tgttggctac tgatgggttg      1260
tgaggagacta tgcataaggca ggatgtgggt aggattgtgg gtgagtacct aactggcatg      1320
catcaccaac agccaatagc tgttggtggc tacaaggtga ctctgggaca gatgcatggc      1380
cttttaacag aaaggagaac caaaatgtcc tcggtatttg aggatcagaa cgcagcaacc      1440
catctcatte gccacgctgt gggcaacaac gagtttggga ctgttgatca tgagcgcctc      1500
tctaaaatgc ttagtcttcc tgaagagctt gctcgaatgt acagagatga cattacaatc      1560
attgtagttc agttcaattc tcatgttgta ggggcgtatc aaaaccaaga a      1611

```

```

<210> 4
<211> 300
<212> PRT

```

<213> Artificial Sequence

<220>

<223> consensus sequence

<400> 4

Leu	Asp	Val	Gly	Val	Ser	Arg	Met	Gln	Gly	Trp	Arg	Lys	Ser	Met	Glu
1				5					10					15	
Asp	Ala	His	Ile	Ala	Leu	Lys	Asn	Leu	Asn	Ser	Ser	Ser	Ser	Gly	Lys
		20					25						30		
Asp	Ser	Trp	Ser	Phe	Phe	Ala	Val	Phe	Asp	Gly	His	Gly	Ser	Gln	Ala
		35				40					45				
Ala	Lys	Tyr	Ala	Gly	Lys	His	Leu	His	Lys	Thr	Ile	Leu	Ala	Glu	Arg
		50				55					60				
Lys	Ser	Phe	Pro	Glu	Gly	Asp	Pro	Trp	Glu	Met	Lys	Leu	Ser	Asp	Leu
65					70					75				80	
Glu	Asp	Ala	Leu	Lys	Glu	Ser	Phe	Leu	Glu	Ala	Asp	Thr	Asp	Glu	Glu
				85					90					95	
Leu	Arg	Ser	Ala	Glu	Ala	Ser	Ala	Ala	Asn	Lys	Val	Leu	Thr	Lys	Glu
			100					105					110		
Asp	Leu	Ser	Ser	Gly	Ser	Thr	Ala	Val	Val	Ala	Leu	Ile	Arg	Gly	Asn
		115					120						125		
Lys	Leu	Tyr	Val	Ala	Asn	Val	Gly	Asp	Ser	Arg	Ala	Val	Leu	Cys	Arg
		130				135					140				
Asn	Gly	Asn	Ala	Ile	Lys	Trp	Ala	Val	Thr	Leu	Thr	Glu	Asp	His	Lys
145					150					155					160
Pro	Ser	Asn	Glu	Asp	Glu	Arg	Glu	Arg	Ile	Glu	Ala	Ala	Gly	Gly	Phe
				165					170					175	
Val	Ser	Arg	Val	Ser	Asn	Gly	Arg	Val	Asn	Gly	Val	Leu	Ala	Val	Ser
			180					185					190		
Arg	Ala	Phe	Gly	Asp	Phe	Glu	Leu	Lys	Pro	Gly	Ser	Lys	Leu	Gly	Pro
		195					200					205			
Glu	Glu	Ser	Leu	Glu	Ala	Asn	Tyr	Glu	Tyr	Ile	Lys	Ser	Pro	Glu	Gln
		210				215					220				
Leu	Val	Thr	Ala	Glu	Pro	Asp	Val	Thr	Ser	Ser	Thr	Asp	Leu	Thr	Pro
225					230					235					240
Asp	Lys	Asp	Glu	Phe	Leu	Ile	Leu	Ala	Cys	Asp	Gly	Leu	Trp	Asp	Val
				245					250					255	
Val	Ser	Asp	Gln	Glu	Val	Val	Asp	Ile	Val	Arg	Ser	Glu	Leu	Ser	Asp
			260					265					270		
Gly	Asn	Lys	Ser	Ala	Glu	Asp	Pro	Met	Glu	Ala	Ala	Glu	Lys	Leu	Val
		275					280						285		
Asp	Glu	Ala	Ile	Ala	Arg	Gly	Ser	Glu	Asp	Asn	Ile				
		290				295					300				

<210> 5

<211> 338

<212> PRT

<213> Artificial Sequence

<220>

<223> consensus sequence

<400> 5

Glu	Ser	Ser	Gly	Lys	Asn	Leu	Gly	Leu	Arg	Tyr	Gly	Leu	Gly	Glu	Ser
1				5					10					15	
Ser	Met	Gln	Gly	Trp	Arg	Lys	Pro	Met	Glu	Asp	Ala	His	Val	Ile	Arg
		20					25					30			
Pro	Phe	Phe	Gly	Val	Phe	Asp	Gly	His	Gly	Gly	Ser	Glu	Ala	Ala	Lys
		35				40						45			
Phe	Leu	Ser	Lys	Asn	Leu	His	Glu	Ile	Leu	Ala	Glu	Glu	Leu	Ser	Phe

50	55	60
Asp Lys Asp Glu Ser Leu Lys Glu Asn Glu Glu Leu Lys Asp Glu Pro		
65	70	75
Glu Ser Ser Glu Arg Leu Asn Gly Asp Lys Ser Leu Glu Asp Val Glu		80
	85	90
Glu Ala Leu Arg Lys Ala Phe Leu Arg Thr Asp Glu Glu Ile Ser Thr		95
	100	105
Ala Val Val Ala Leu Ile Arg Gly Asn Lys Leu Tyr Val Ala Asn Val		110
	115	120
Gly Asp Ser Arg Ala Val Leu Cys Arg Asn Gly Lys Asp Ser Trp Glu		125
	130	135
Gly Val Arg Thr Tyr Ser Ala Val Gln Leu Thr Glu Asp His Lys Pro		140
145	150	155
Ser Asn Glu Asp Glu Arg Glu Arg Ile Glu Ala Ala Gly Gly Glu Val		160
	165	170
Glu Pro Ile Asp Arg Glu Phe Val Ser Asn Gly Gly Gly Val Val Trp		175
	180	185
Arg Val Asn Gly Val Val Ile Ser Leu Ala Val Ser Arg Ala Leu Gly		190
	195	200
Asp Phe Glu Leu Lys Lys Lys Glu Asp Glu Leu Ile Glu Glu Asn Arg		205
	210	215
Leu Tyr Glu Lys Phe Asp Pro Arg Leu Pro Gly Lys Glu Pro Tyr Val		220
225	230	235
Ser Ala Glu Pro Glu Val Thr Val Val Glu Leu Ser Gln Thr Leu Val		240
	245	250
Pro Thr Glu Asp Asp Phe Leu Ile Leu Ala Ser Asp Gly Leu Trp		255
	260	265
Asp Val Leu Ser Asn Gln Glu Ala Val Asp Ile Val Arg Lys His Leu		270
	275	280
Arg Lys Gly Asp Asp Lys Glu Val Lys Ser Ala Ala Gln Glu Leu Ala		285
	290	295
Arg Ala Asp Ser Leu Arg Ser Lys Lys His Asn Asp Pro Lys Glu Ala		300
305	310	315
Ala Lys Leu Leu Val Asp Leu Ala Leu Lys Asp Asn Ile Thr Val Val		320
	325	330
		335
Val Val		

09801257 070901